

L9	1	I8 and (fulgidus)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/06/16 12:22
L10	2	("20030049643").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 12:23
L11	2	("20030049634").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 12:25
L12	2	("5556772").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 12:25
S1	2	("6713071").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/15 19:01
S2	2	("4693980").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/15 19:02
S3	2	("6881559").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/15 19:02
S4	2	("5453372").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 11:02

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	7672	exonuclease same polymerase	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:03
L2	37	I1 and ((enhanc\$4 fidelity increas\$) near exonuclease)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:38
L3	15	I2 and ((composition combination) same (exonuclease))	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:48
L4	2	("6482590").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 11:49
L5	1502	(composition mixture combination) near5 (polymerase and exonuclease)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:50
L6	0	I5 and fulgidis	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:50
L7	39	I5 and fulgidus	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/16 11:51
L8	2	("5843669").PN.	US-PGPUB; USPAT; USOCR; EPO; DERWENT	OR	OFF	2005/06/16 11:52

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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:18:10 ; Search time 157 Seconds  
(without alignments)  
628.553 Million cell updates/sec

Title: US-09-856-850A-18  
Perfect score: 257  
Sequence: 1 MLKIATFNVNSIRSRLHIVI.....KPRLAEKPSDHLPLVAVFDV 257

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1714042 seqs, 383979560 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:12:09 ; Search time 488 Seconds  
(without alignments)  
615.118 Million cell updates/sec

Title: US-09-856-850A-18  
Perfect score: 257  
Sequence: 1 MLKIATFNVNSIRSRLHIVI.....KPRLAEKPSDHLPLVAVFDV 257

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 6959266 seqs, 1168006243 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*
- 7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*
- 8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*
- 9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*
- 10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*
- 11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*
- 12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*
- 13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*
- 14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*
- 15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*
- 16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*
- 17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*
- 18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*
- 19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*
- 20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*
- 21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep:\*
- 22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep:\*
- 23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*
- 24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep:\*
- 25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep:\*
- 26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*
- 27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*
- 28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*
- 29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*
- 30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*
- 31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep:\*
- 32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*
- 33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep:\*
- 34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep:\*

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35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep:\*  
36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep:\*  
37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Run on: June 16, 2005, 12:14:59 ; Search time 60 Seconds  
(without alignments)  
526.230 Million cell updates/sec

Title: US-09-856-850A-18  
Perfect score: 257  
Sequence: 1 MLKIATFNVNSIRSRLHIVI.....KPRLAEKPSDHLPLVAVFDV 257

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 578766 seqs, 122855171 residues

Word size : 0

Total number of hits satisfying chosen parameters: 578766

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.